

SEQUENCE LISTING

<110> Isis Pharmaceuticals, Inc.
 National University of Singapore
 Monia, Brett P.
 Dobie, Kenneth W.
 Freier, Susan M.
 Popoff, Ian
 Wong, Wai Shiu Fred
 Karras, James G.

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 Activated Protein Kinase Expression

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 Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys
 1 5 10 15

aca atc tgg gag gtg ccc gag cgt tac cag aac ctg tct cca gtg ggc 455
 Thr Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly
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tct ggc gcc tat ggc tct gtg tgt gct gct ttt gac aca aaa acg ggg 503
 Ser Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly
 35 40 45

tta cgt gtg gca gtg aag aag ctc tcc aga cca ttt cag tcc atc att 551
 Leu Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile
 50 55 60

cat gcg aaa aga acc tac aga gaa ctg cgg tta ctt aaa cat atg aaa 599
 His Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys
 65 70 75

cat gaa aat gtg att ggt ctg ttg gac gtt ttt aca cct gca agg tct 647
 His Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser
 80 85 90 95

ctg gag gaa ttc aat gat gtg tat ctg gtg acc cat ctc atg ggg gca 695
 Leu Glu Glu Phe Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala
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 Met Ser Gln
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 Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr Ile Trp Glu
 5 10 15

gtg ccc gaa cga tac cag aac ctg tcc ccg gtg ggc tcg ggc gcc tat 334
 Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser Gly Ala Tyr
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Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His Ala Lys Arg
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acc tac cga gag ttg cgt ctg ctg aag cac atg aaa cac gaa aat gtg 478
Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His Glu Asn Val
      70                      75                      80

att ggt ctg ttg gat gtg ttc aca ccc gca agg tca ctg gag gaa ttc 526
Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu Glu Glu Phe
      85                      90                      95

aat gac gtg tac ctg gtg acc cat ctc atg ggg gcg gac ctg aac aac 574
Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala Asp Leu Asn Asn
    100                      105                      110                      115

atc gtg aag tgc cag aag ctg acc gac gac cac gtt cag ttt ctc atc 622
Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln Phe Leu Ile
      120                      125                      130

tac cag atc ctc cga ggg ctg aag tat ata cat tgc gct gac ata att 670
Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asp Ile Ile
      135                      140                      145

cac agg gac cta aag ccc agc aac cta gct gtg aac gaa gac tgt gag 718
His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu Asp Cys Glu
      150                      155                      160

ctc aag att ctg gat ttt ggg ctg gct cgg cac act gat gat gag atg 766
Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp Asp Glu Met
      165                      170                      175

aca ggc tac gtg gct acc agg tgg tac cga gcc cca gag atc atg ctg 814
Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu
    180                      185                      190                      195

aat tgg atg cac tat aac cag aca gtg gat att tgg tcc gtg ggc tgc 862
Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser Val Gly Cys
      200                      205                      210

atc atg gct gag ctg ttg acc gga aga acg ttg ttt cct ggt aca gac 910
Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro Gly Thr Asp
      215                      220                      225

cat att aac cag ctt cag cag ata atg cgt atg acg ggg aca ccc cct 958
His Ile Asn Gln Leu Gln Gln Ile Met Arg Met Thr Gly Thr Pro Pro
      230                      235                      240

gct tat ctc att aac agg atg cca agc cat gag gca aga aac tac att 1006
Ala Tyr Leu Ile Asn Arg Met Pro Ser His Glu Ala Arg Asn Tyr Ile
      245                      250                      255

cag tct ctg gcc cag atg ccg aag atg aac ttc gca aat gta ttt att 1054
Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn Val Phe Ile
    260                      265                      270                      275

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ggt gcc aat ccc ctg gct gtc gac cta ctg gag aag atg ctc gtt ttg 1102
 Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met Leu Val Leu
 280 285 290

gac tca gat aag agg atc aca gca gcc caa gct ctt gcg cat gcc tac 1150
 Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala His Ala Tyr
 295 300 305

ttt gct cag tac cac gac cct gat gat gag cct gtt gct gac cct tat 1198
 Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala Asp Pro Tyr
 310 315 320

gac cag tcc ttt gaa agc agg gac ctt ctc ata gat gag tgg aag agc 1246
 Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu Trp Lys Ser
 325 330 335

ctg acc tat gat gaa gtc atc agc ttt gtg cca cca ccc ctt gac caa 1294
 Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro Leu Asp Gln
 340 345 350 355

gaa gaa atg gag tcc tga gcacctgggt tctgtttctgt ctatctcact 1342
 Glu Glu Met Glu Ser
 360

tcaactgtgag gggaagacct tctcatggga actctccaaa taccattcaa gtgcctcttg 1402
 ttgaaagatt ccttcatggg ggaagggggg gcatgtatgt gttagtgttt gtgtgtgtgt 1462
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 tttatgagtt gtgaatgggc cttggcagtc tgccctgttt ctgagagtct gggcaggccg 1582
 atgggaactg tcatctcctt agggatgtgt gtgttcagtg caaagtaaga aatatgaaaa 1642
 tatccctgtt cttagttacc ttgccacttt ggcttctcct gtggccctgc ctttaccata 1702
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 aagagaacca actggctcct ggtctctagc ctgtgaccgg cttgcttaat gtccctcagaa 1822
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 tggatggcca gtggggagct ggaaaaaaca aggcagcctt taggaaggcc atggtgcatg 2002
 tgtgtgcatg cgtgtatgtg cagccgccct cctcacttc aggagcaagc tgtttgctgt 2062
 gcttaccctt cacctcagtg cagaggtctc cagtgccgag cacaggcacc tgccatcagt 2122
 agttcctgtg tcatcttcac atctagcaga gcacggatgt gtttgcatgc tgtgctcttg 2182
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 ctactttgtg ttgaacacaa ttgattctcc aggtgctcat ggtgcaggaa aacaggacag 2362
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 agggcaaat attttaatat tttgtatgtt cacctttata aacatgaatc ctgaggggtg 2782
 aagaactgtt tgcataatgt tctgaatgtt gagcactttg tgctatataa ggaccatata 2842
 ttaagctttg tgtgcagtaa gaaagtgtaa agccaattcc agtgttgagc gtgacaggtc 2902
 ttgtgttttag gtcaagggtg ctctctcag tgcagggaca tgcctgctct gtggggcagg 2962
 cgaggaccct gaatcatttg gagcccagaa ggaggcagac tggccaggtc tcaccacctc 3022
 agtgtgcagt tcaactccat gccatcccat caagatgggt tagtagcagt gtctgttttt 3082
 gaatgccaag tgtgatttcc aacaattctg ctctgggtat ttcattgaag acatctttgc 3142
 acatgtgacc atgctgtgtt aggggctgtg ttccagggac tggactcgaa gctagaactg 3202
 gcagaagagt tctggcatcc acagcgcaat gctgccacca cccagtttct tcatcagaag 3262
 acaagggaac gagaaaactg ctgttcgttt gtatttgtga acttggtgt aatctggtat 3322
 gccataggat gtcagataat accactgggt 3352

<210> 169

<211> 503
 <212> DNA
 <213> M. musculus

<400> 169
 cgcaagaata aagtcagtgg tcacaaatag aggggggtcag tggctagaag aagagtaagc 60
 ctgaattgag catcccagac agtgggtccat acggggccgtc agctagctca ttccctgaga 120
 tcactaacac tactgaacat agtcattctg aaagtctgtg tttttacagg caagaaacta 180
 cattcagtct ctggcccag atg ccg aag atg aac ttc gca aat gta ttt att 232
 ggt gcc aat ccc ctg gct gtc gac cta ctg gag aag atg ctc gtt ttg 280
 gac tca gat aag agg atc aca gca gcc caa gct ctt gcg cat gct act 328
 ttg ctc agt acc acg acc ctg atg atg agc ctg ttg ctg acc ctt atg 376
 acc agt cct ttg aaa gca ggg acc ttc tca tag atgagtggaa gagcctgacc 429
 tatgatgaag tcatcagctt tgtgccacca ccccttgacc aagaagagat ggagtcctga 489
 gcacctgggtt tctg 503

<210> 170
 <211> 1500
 <212> DNA
 <213> M. musculus

<220>
 <221> CDS
 <222> (297)...(1073)

<400> 170
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 cggctgcagg aggaccgcgg cgggagcagc ctcgagccgt gcagccggct ccggcacctt 120
 gccgacgctc gtaggagccg ccgcggctga caggggcgcg gggtcgcagc ctccacacct 180
 gcgcgggttg cgggcgcggg gtccgggtctg ccgcgggcgg gcgcagagga gagcgtgcgg 240
 ctgcaggcag gagccccgc tcggccacct cctcgccccg ctgctgccgc tggaag atg 299
 Met
 1
 tcg cag gag agg ccc acg ttc tac cgg cag gag ctg aac aag acc atc 347
 Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr Ile
 5 10 15
 tgg gag gtg ccc gaa cga tac cag aac ctg tcc ccg gtg ggc tcg ggc 395
 Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser Gly
 20 25 30
 gcc tat ggc tcg gtg tgt gct gct ttt gat aca aag acg ggg cat cgt 443
 Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His Arg
 35 40 45
 gtg gca gtt aag aag ctg tcg aga ccg ttt cag tcc atc att cac gcc 491
 Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His Ala
 50 55 60 65
 aaa agg acc tac cga gag ttg cgt ctg ctg aag cac atg aaa cac gaa 539
 Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His Glu
 70 75 80
 aat gtg att ggt ctg ttg gat gtg ttc aca ccc gca agg tca ctg gag 587
 Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu Glu
 85 90 95
 gaa ttc aat gac gtg tac ctg gtg acc cat ctc atg ggg gcg gac ctg 635
 Glu Phe Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala Asp Leu

100	105	110	
aac aac atc gtg aag tgc cag aag ctg acc gac gac cac gtt cag ttt			683
Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln Phe			
115	120	125	
ctc atc tac cag atc ctc cga ggg ctg aag tat ata cat tcg gct gac			731
Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asp			
130	135	140	145
ata att cac agg gac cta aag ccc agc aac cta gct gtg aac gaa gac			779
Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu Asp			
	150	155	160
tgt gag ctc aag att ctg gat ttt ggg ctg gct cgg cac act gat gat			827
Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp Asp			
	165	170	175
gag atg aca ggc tac gtg gct acc agg tgg tac cga gcc cca gag atc			875
Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Ile			
	180	185	190
atg ctg aat tgg atg cac tat aac cag aca gtg gat att tgg tcc gtg			923
Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser Val			
	195	200	205
ggc tgc atc atg gct gag ctg ttg acc gga aga acg ttg ttt cct ggt			971
Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro Gly			
	210	215	220
aca gac cat att gat cag ttg aag ctc att tta aga ctc gtt gga acc			1019
Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly Thr			
	230	235	240
cca ggg gct gag ctt ctg aag aaa atc tcc tca gag tct gat gcc aag			1067
Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Asp Ala Lys			
	245	250	255
cca tga ggtgagaaca aacagcatgc acaggggaagt ctacctcgga ggccaccttc			1123
Pro			
tcgtagtagt gtctgtgtat agccagcagt ttctaattgtc accgaatgct tgcattgtcc			1183
ccaagaaccg ttaaagcagt actggctgtg tgctagcgga gtgttggcat ttaggatgca			1243
gtctcctgag cctgagaggc agcgatgcag tgtagggcag tggtccctag tggttggtt			1303
tctgatcttg tgcttgaggt aacaagtgtc gttgcagttg tatgtagtta gggtgtgcta			1363
cagccgtgtc atgggtgcat ggaacagagt tcattagtgt gctttgctct ccacccattt			1423
tacaaccaag agaagactgc atgcaagcac gcactataaa attccttgtg ctaataaaaa			1483
aaaaaaaaa aaaaaaa			1500

<210> 171

<211> 384

<212> DNA

<213> M. musculus

<400> 171

ttgcaaggac gctccagctc gccgcttagt cacataccac tgctcatttc agtattgttt 60
 gacaaaacag ttttccatac cgagcagagg ggcgcccctc aagatcaaga agtgctgctt 120
 ttgatacaaa gacggggcat cgtgtggcag ttaagaagct gtcgagaccg tttcagtcca 180
 tcattcacgc caaaaggacc taccgagagt tgcgtctgct gaagcacatg aaacacgaaa 240

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atgtgattgg tctgttggat gtgttcacac ccgcaaggct actggaggaa ttcaatgacg 300
tgtacctggg gacctatctc atgggggcgg acctgaacaa catcgtgaag tgccagaagc 360
tgaccgacga ccacgttcag tttc                                     384

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<210> 172

<211> 463

<212> DNA

<213> M. musculus

<220>

<221> misc_feature

<222> 429

<223> n = A, T, C, or G

<400> 172

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cgcgagaggc tcccggccgc tgcctgtggg atcgccgcca ctggagccca agcggggcgc 120
tgaagcgcga gcgggtgtct tgccggcgtc gcgtgcgctc cctccccggg gagcggctgc 180
aggaggaccg cggcggggagc agcctcgagc cgtgcagccg gctccggcac cttgccgacg 240
ctcgtaggag ccgcgcgcgc tgacaggggc ggccgggtcgc accctccaca cctgcgcggg 300
tgccgggcgc ggggtccggt ctgccgcggg cgggcgcaga ggagagcgtg cggctgcagg 360
caggagcccc cgctcgccca cctcctcgcc ccgctgctgc cgctggaaga tgtcgcagga 420
gaggcccang ttctaccggc aggagctgaa caagaccatc tgg                                     463

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<210> 173

<211> 1083

<212> DNA

<213> R. norvegicus

<220>

<221> CDS

<222> (1)...(1083)

<400> 173

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atg tct cag gag agg ccc acg ttc tac cgg cag gag ctg aac aag acc 48
Met Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr
  1          5          10          15

gtc tgg gag gtg ccc gag cga tac cag aac ctg tcc ccg gtg ggc tcg 96
Val Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
          20          25          30

gga gcc tac ggc tcg gtg tgt gct gct ttt gat aca aag acg gga cat 144
Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly His
          35          40          45

cgt gtg gca gtg aag aag ctg tcg aga ccg gtt cag ccc atc att cac 192
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Val Gln Pro Ile Ile His
          50          55          60

gcc aaa agg tcc tac agg gag ctg cgg ctg ctg aag cac atg aag cac 240
Ala Lys Arg Ser Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His
          65          70          75          80

gag aat gtg att ggt ctg ttg gat gtg ttt aca cct gca agg tcc ctg 288
Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
          85          90          95

gag gaa ttc aac gat gtg tac ctg gtg acc cat ctc atg ggg gca gac 336

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Glu Glu Phe Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala Asp	
100 105 110	
ctg aac aac atc gtg aag tgt cag aag ctt acc gat gac cac gtt cag	384
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln	
115 120 125	
ttt ctt atc tac cag atc ctg cga ggg ctg aag tat ata cac tcg gct	432
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala	
130 135 140	
gac ata atc cac agg gac cta aag ccc agc aac ctc gct gtg aat gaa	480
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu	
145 150 155 160	
gac tgt gag ctg aag att ctg gat ttt ggg ctg gct cgg cac act gat	528
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp	
165 170 175	
gac gaa atg acc ggc tac gtg gct acc cgg tgg tac aga gcc ccc gag	576
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu	
180 185 190	
att atg ctg aat tgg atg cac tac aac cag aca gtg gat att tgg tcc	624
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser	
195 200 205	
gtg ggc tgc atc atg gct gag ctg ttg acc gga aga acg ttg ttt cct	672
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro	
210 215 220	
ggg aca gac cat att gat cag ttg aag ctc att tta aga ctc gtt gga	720
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly	
225 230 235 240	
acc cca ggg gct gag ctt ctg aag aaa atc tcc tca gag tct gca aga	768
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg	
245 250 255	
aac tac att cag tct ctg gcc cag atg ccg aag atg aac ttc gca aat	816
Asn Tyr Ile Gln Ser Leu Ala Gln Met Pro Lys Met Asn Phe Ala Asn	
260 265 270	
gta ttt att ggt gcc aat ccc ctg gct gtc gac ctg ctg gaa aag atg	864
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met	
275 280 285	
ctg gtt ttg gac tca gat aag agg atc aca gca gcc caa gct ctt gcg	912
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala	
290 295 300	
cat gcc tac ttt gct cag tac cac gac cct gat gat gag cca gtg gct	960
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala	
305 310 315 320	
gac cct tat gac cag tcc ttt gaa agc agg gac ctc ctt ata gac gaa	1008
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu	
325 330 335	
tgg aag agc ctg acc tac gat gaa gtc att agc ttt gtg cca ccg ccc	1056
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro	

340 345 350 1083

ctt gac caa gaa gaa atg gac tcc tga
Leu Asp Gln Glu Glu Met Asp Ser
355 360

<210> 174
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 174
gtgcgcgcgga gcccgaaatc 20

<210> 175
<211> 20
<212> DNA
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<220>
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<400> 175
ctgcgacatt ttccagcggc 20

<210> 176
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 176
catcatcagg gtcgtggtac 20

<210> 177
<211> 20
<212> DNA
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<220>
<223> Antisense Oligonucleotide

<400> 177
aggtgctcag gactccatct 20

<210> 178
<211> 20
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<220>

<223> Antisense Oligonucleotide

<400> 178

gtccctgctt tcaaaggact

20

<210> 179

<211> 20

<212> DNA

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<210> 180

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 180

agctcctgcc ggtagaacgt

20

<210> 181

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 181

tcaaaagcag cacacaccga

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<210> 182

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cccgtctttg tatcaaaagc

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<210> 183

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<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 183
aacggtctcg acagcttctt

20

<210> 184
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 184
taggtccttt tggcgtgaat

20

<210> 185
<211> 20
<212> DNA
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<220>
<223> Antisense Oligonucleotide

<400> 185
agatgggtca ccaggtacac

20

<210> 186
<211> 20
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<220>
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<400> 186
gcccccatga gatgggtcac

20

<210> 187
<211> 20
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<220>
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<400> 187
tcatacgtgt gccgagccag

20

<210> 188
<211> 20
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<400> 188
gtcaacagct cagccatgat

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<210> 189
<211> 20
<212> DNA
<213> Artificial Sequence

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<400> 189
cgttcttccg gtcaacagct

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<210> 190
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<400> 190
atcaatatgg tctgtaccag

20

<210> 191
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<400> 191
cttaaaatga gcttcaactg

20

<210> 192
<211> 20
<212> DNA
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<220>
<223> Antisense Oligonucleotide

<400> 192
gggtccaac gagtcttaaa

20

<210> 193
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 193

tcagaagctc agcccctggg

20

<210> 194

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 194

ggagattttc ttcagaagct

20

<210> 195

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 195

cagactctga ggagattttc

20

<210> 196

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 196

tagtttcttg cagactctga

20

<210> 197

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 197

agactgaatg tagtttcttg

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<210> 198

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 198

ttcatcttcg gcatctgggc

20

<210> 199
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 199
atttgcggaag ttcattcttcg 20

<210> 200
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Antisense Oligonucleotide

<400> 200
caataaatac atttgcggaag 20

<210> 201
<211> 20
<212> DNA
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<223> Antisense Oligonucleotide

<400> 201
ggattggcac caataaatac 20

<210> 202
<211> 20
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<220>
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<400> 202
gctgctgtga tcctcttatac 20

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